

SEQUENCE LISTING

<110> Lunden, Anne
Andersson, Leif
Marklund, Stefan

<120> Detection of Mutations

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<150> PCT/IB03/00028

<151> 2003-01-09

<150> PA 2002 00031

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tgt ttt cca gac ttt cca ttt cct gat gat ttt cct aac ttt atg cac      97
Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn Phe Met His
          20             25             30

aac agc aag ctc cag gaa tat att act atg ttt gcc aaa gaa aag      142
Asn Ser Lys Leu Gln Glu Tyr Ile Thr Met Phe Ala Lys Glu Lys
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    1             5             10             15

ctg ttt atc act cga ttt gaa aca ttc ctc aag aac acc tta ccg aca      97
Leu Phe Ile Thr Arg Phe Glu Thr Phe Leu Lys Asn Thr Leu Pro Thr
          20             25             30

gtc att tct aac tgg tgg tac atg aag caa atg aac gcc aga ttc aag      145
Val Ile Ser Asn Trp Trp Tyr Met Lys Gln Met Asn Ala Arg Phe Lys
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cac gag      151
His Glu
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 att aag cca aat gtg aag gag ttt aca gag gat tca gct att ttt gag 97
 Ile Lys Pro Asn Val Lys Glu Phe Thr Glu Asp Ser Ala Ile Phe Glu
 20 25 30

 gat ggg acg gtg ttt aag gcc att gac tat gtc atc ttt gca aca ggc 145
 Asp Gly Thr Val Phe Lys Ala Ile Asp Tyr Val Ile Phe Ala Thr Gly
 35 40 45

 tat agt tat gcc tac ccc ttc ctt gat gac tcc atc att aag agc aga 193
 Tyr Ser Tyr Ala Tyr Pro Phe Leu Asp Asp Ser Ile Ile Lys Ser Arg
 50 55 60

 gac aat gag gtc acc tta ttt aaa ggc ata ttc cca cct cca ctg gaa 241
 Asp Asn Glu Val Thr Leu Phe Lys Gly Ile Phe Pro Pro Pro Leu Glu
 65 70 75 80

 aag cca acc ttg gct gtg atc ggc ctt gtc cag tcc ctt gga gct gcc 289
 Lys Pro Thr Leu Ala Val Ile Gly Leu Val Gln Ser Leu Gly Ala Ala
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 gag ctt gcc tcc ttc att ggg gca aag ccc aac atc cca tgg ctg ttt 97
 Glu Leu Ala Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro Trp Leu Phe
 20 25 30

ctc aca gat cca aag ttg gca ttg gag gtc tac ttt ggc cct tgc acc 145
 Leu Thr Asp Pro Lys Leu Ala Leu Glu Val Tyr Phe Gly Pro Cys Thr
 35 40 45

cca tac cag ttt agg ctg gtg ggc cca gga aag tgg cca gga gcc aga 193
 Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Lys Trp Pro Gly Ala Arg
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 Asn Ala Ile
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 tagaccacta aatcctgttt cagccctcca tatctcctgc aatatatcat aaaagagaga 240
 cccagaaaga ttaaatttca gaggagcttg ggaacacacg gatgtggact tctattttct 300
 agctcataca tcctctaaaa tgtaaggatg ccttccaata ggtggctcta ataaatgact 360
 cagccacaca acaactagtc agaagaacta ggctccagtc ctacctctgt cactaatcag 420
 ctcagtggcc atgaattaat aactacacgt gagcaagaga caattcctct acttgtaaata 480
 gtggataaaa atgcctttct cagcagcctt gttgtgttgt ggaatgtcca agtgagatca 540
 gtatgaaagt ccttcagtaa aatctacaaa gtactggata atgagcaata atccccttac 600
 caacaaaagg atcgatgttg atttgcgtgg ataaaaagggt gtgaggcatt ttccctgttc 660
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 Ile Ser Gly Leu Ala Ser Ile Arg Asn Cys Leu Glu Glu Gly Leu Glu
 15 20 25

 ccc acc tgc ttt gag aag ggt gaa gac att ggg ggc ctg tgg aaa ttc 146
 Pro Thr Cys Phe Glu Lys Gly Glu Asp Ile Gly Gly Leu Trp Lys Phe
 30 35 40

 tcg gac cat gta gag gaa ggc agg gcc agc att tat cgg tca gtc ttt 194
 Ser Asp His Val Glu Glu Gly Arg Ala Ser Ile Tyr Arg Ser Val Phe
 45 50 55

 acc aac tct tcc aaa gag atg aca tgt ttt cca gac ttt cca ttt cct 242
 Thr Asn Ser Ser Lys Glu Met Thr Cys Phe Pro Asp Phe Pro Phe Pro
 60 65 70 75

 gat gat ttt cct aac ttt atg cac aac agc aag ctc cag gaa tat att 290
 Asp Asp Phe Pro Asn Phe Met His Asn Ser Lys Leu Gln Glu Tyr Ile
 80 85 90

 act atg ttt gcc aaa gaa aag aac ctc ctg aaa tac ata caa ttt aag 338
 Thr Met Phe Ala Lys Glu Lys Asn Leu Leu Lys Tyr Ile Gln Phe Lys
 95 100 105

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 aca att gta tcc agt gta aat aag cgt ccc gat ttc caa acc act ggc 386
 Thr Ile Val Ser Ser Val Asn Lys Arg Pro Asp Phe Gln Thr Thr Gly
 110 115 120

 caa tgg gat gtt atc act gaa aag gat ggt aaa aag gaa tca gct gtc 434
 Gln Trp Asp Val Ile Thr Glu Lys Asp Gly Lys Lys Glu Ser Ala Val
 125 130 135

 ttt gat gcc gta atg att tgt tct gga cat cat gtg tac ccc aac ata 482

Phe Asp Ala Val Met Ile Cys Ser Gly His His Val Tyr Pro Asn Ile	
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Pro Lys Glu Ser Phe Pro Gly Ile Lys Leu Phe Lys Gly Lys Cys Phe	
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His Ser Arg Asp Tyr Lys Glu Pro Gly Ile Phe Lys Gly Lys Arg Val	
175 180 185	
ctg gtg att ggt ctg ggg aac tca ggc tgt gac atc gcc tca gaa ctc	626
Leu Val Ile Gly Leu Gly Asn Ser Gly Cys Asp Ile Ala Ser Glu Leu	
190 195 200	
agc cac ata gct gaa aaa gtc atc atc agc tcc cga agt ggc tcc tgg	674
Ser His Ile Ala Glu Lys Val Ile Ile Ser Ser Arg Ser Gly Ser Trp	
205 210 215	
gtg atg agc cgg gtc tgg gat gaa ggc tat cca tgg gac atg ctg ttt	722
Val Met Ser Arg Val Trp Asp Glu Gly Tyr Pro Trp Asp Met Leu Phe	
220 225 230 235	
atc act cga ttt gaa aca ttc ctc aag aac acc tta ccg aca gtc att	770
Ile Thr Arg Phe Glu Thr Phe Leu Lys Asn Thr Leu Pro Thr Val Ile	
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tct aac tgg tgg tac atg aag caa atg aac gcc aga ttc aag cac gag	818
Ser Asn Trp Trp Tyr Met Lys Gln Met Asn Ala Arg Phe Lys His Glu	
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Asn Tyr Gly Leu Met Pro Leu Asn Ser Thr Leu Arg Lys Glu Pro Val	
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Phe Asn Asp Glu Leu Pro Ala Cys Ile Leu Cys Gly Ile Val Thr Ile	
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Lys Pro Asn Val Lys Glu Phe Thr Glu Asp Ser Ala Ile Phe Glu Asp	
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Gly Thr Val Phe Lys Ala Ile Asp Tyr Val Ile Phe Ala Thr Gly Tyr	
320 325 330	
agt tat gcc tac ccc ttc ctt gat gac tcc atc att aag agc aga gac	1058
Ser Tyr Ala Tyr Pro Phe Leu Asp Asp Ser Ile Ile Lys Ser Arg Asp	
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Asn Glu Val Thr Leu Phe Lys Gly Ile Phe Pro Pro Pro Leu Glu Lys	
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Pro Thr Leu Ala Val Ile Gly Leu Val Gln Ser Leu Gly Ala Ala Ile	
365 370 375	
ccc act act gac ctg cag tct cgc tgg gca gta caa gta att aag gga	1202
Pro Thr Thr Asp Leu Gln Ser Arg Trp Ala Val Gln Val Ile Lys Gly	
380 385 390 395	
aca tgc cct ttg cct tct gtc aag gac atg atg aat gat att gat gaa	1250
Thr Cys Pro Leu Pro Ser Val Lys Asp Met Met Asn Asp Ile Asp Glu	
400 405 410	
aaa atg ggg aaa aag ctc aaa ttg ttt ggc aaa agt gat acc ata cag	1298
Lys Met Gly Lys Lys Leu Lys Leu Phe Gly Lys Ser Asp Thr Ile Gln	
415 420 425	
acg gat tat gtt gtt tat atg gat gag ctt gcc tcc ttc att ggg gca	1346
Thr Asp Tyr Val Val Tyr Met Asp Glu Leu Ala Ser Phe Ile Gly Ala	
430 435 440	
aag ccc aac atc cca tgg ctg ttt ctc aca gat cca aag ttg gca ttg	1394
Lys Pro Asn Ile Pro Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Leu	
445 450 455	
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Glu Val Tyr Phe Gly Pro Cys Thr Pro Tyr Gln Phe Arg Leu Val Gly	
460 465 470 475	
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Pro Gly Lys Trp Pro Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp	
480 485 490	
cgg tta ctg aaa cct atg acg aca aga gtg gtt ggg agt cct ctg aag	1538
Arg Leu Leu Lys Pro Met Thr Thr Arg Val Val Gly Ser Pro Leu Lys	
495 500 505	
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Pro Cys Leu Phe Cys Asn Trp Phe Arg Pro Val Leu Ile Ser Val Val	
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Lys	Gly	Glu	Asp	Ile	Gly	Gly	Leu	Trp	Lys	Phe	Ser	Asp	His	Val	Glu	35	40	45	
Glu	Gly	Arg	Ala	Ser	Ile	Tyr	Arg	Ser	Val	Phe	Thr	Asn	Ser	Ser	Lys	50	55	60	
Glu	Met	Thr	Cys	Phe	Pro	Asp	Phe	Pro	Phe	Pro	Asp	Asp	Phe	Pro	Asn	65	70	75	80
Phe	Met	His	Asn	Ser	Lys	Leu	Gln	Glu	Tyr	Ile	Thr	Met	Phe	Ala	Lys	85	90	95	
Glu	Lys	Asn	Leu	Leu	Lys	Tyr	Ile	Gln	Phe	Lys	Thr	Ile	Val	Ser	Ser	100	105	110	
Val	Asn	Lys	Arg	Pro	Asp	Phe	Gln	Thr	Thr	Gly	Gln	Trp	Asp	Val	Ile	115	120	125	
Thr	Glu	Lys	Asp	Gly	Lys	Lys	Glu	Ser	Ala	Val	Phe	Asp	Ala	Val	Met	130	135	140	
Ile	Cys	Ser	Gly	His	His	Val	Tyr	Pro	Asn	Ile	Pro	Lys	Glu	Ser	Phe	145	150	155	160
Pro	Gly	Ile	Lys	Leu	Phe	Lys	Gly	Lys	Cys	Phe	His	Ser	Arg	Asp	Tyr	165	170	175	
Lys	Glu	Pro	Gly	Ile	Phe	Lys	Gly	Lys	Arg	Val	Leu	Val	Ile	Gly	Leu	180	185	190	
Gly	Asn	Ser	Gly	Cys	Asp	Ile	Ala	Ser	Glu	Leu	Ser	His	Ile	Ala	Glu	195	200	205	
Lys	Val	Ile	Ile	Ser	Ser	Arg	Ser	Gly	Ser	Trp	Val	Met	Ser	Arg	Val	210	215	220	
Trp	Asp	Glu	Gly	Tyr	Pro	Trp	Asp	Met	Leu	Phe	Ile	Thr	Arg	Phe	Glu	225	230	235	240

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 260 265 270
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 Pro Ala Cys Ile Leu Cys Gly Ile Val Thr Ile Lys Pro Asn Val Lys
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 Glu Phe Thr Glu Asp Ser Ala Ile Phe Glu Asp Gly Thr Val Phe Lys
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 Ala Ile Asp Tyr Val Ile Phe Ala Thr Gly Tyr Ser Tyr Ala Tyr Pro
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 Trp Leu Phe Leu Thr Asp Pro Lys Leu Ala Leu Glu Val Tyr Phe Gly
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 Pro Cys Thr Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Lys Trp Pro
 465 470 475 480
 Gly Ala Arg Asn Ala Ile Leu Thr Gln Trp Asp Arg Leu Leu Lys Pro
 485 490 495
 Met Thr Thr Arg Val Val Gly Ser Pro Leu Lys Pro Cys Leu Phe Cys
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